



**Supplemental Figure S19. Alignments of orthologous and paralogous genes produce characteristically distinct distributions of divergence between samples and phylogenetic tree shapes.** (A, B) Histograms of the divergence of all pairs of samples in two 1kb regions for a typical orthologous region (A) and a region identified as paralogous by our method (B). (C, D) Unrooted neighbor joining (Saitou and Nei 1987; Boc et al. 2012) phylogenies constructed from each of the above loci - (C) A typical locus phylogeny, (D) a phylogeny with two clearly divergent groups of sequences that do not correspond to clades identified in previous phylogenetic studies (Jarvis et al. 2014) and therefore predicted to be the result of a paralogous alignment.